

Lutz Krause

List of Publications by Year in descending order

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Version: 2024-02-01

84
papers

9,963
citations

53794

45
h-index

53230

85
g-index

87
all docs

87
docs citations

87
times ranked

16339
citing authors

#	ARTICLE	IF	CITATIONS
1	The Subsystems Approach to Genome Annotation and its Use in the Project to Annotate 1000 Genomes. <i>Nucleic Acids Research</i> , 2005, 33, 5691-5702.	14.5	1,806
2	Calypso: a user-friendly web-server for mining and visualizing microbiome–environment interactions. <i>Bioinformatics</i> , 2017, 33, 782-783.	4.1	627
3	The coral core microbiome identifies rare bacterial taxa as ubiquitous endosymbionts. <i>ISME Journal</i> , 2015, 9, 2261-2274.	9.8	548
4	Microbial Ecology of Four Coral Atolls in the Northern Line Islands. <i>PLoS ONE</i> , 2008, 3, e1584.	2.5	383
5	Complete genome sequence of the myxobacterium <i>Sorangium cellulosum</i> . <i>Nature Biotechnology</i> , 2007, 25, 1281-1289.	17.5	354
6	Colonization-Induced Host-Gut Microbial Metabolic Interaction. <i>MBio</i> , 2011, 2, e00271-10.	4.1	342
7	The metagenome of a biogas-producing microbial community of a production-scale biogas plant fermenter analysed by the 454-pyrosequencing technology. <i>Journal of Biotechnology</i> , 2008, 136, 77-90.	3.8	329
8	Phylogenetic characterization of a biogas plant microbial community integrating clone library 16S-rDNA sequences and metagenome sequence data obtained by 454-pyrosequencing. <i>Journal of Biotechnology</i> , 2009, 142, 38-49.	3.8	248
9	Phylogenetic classification of short environmental DNA fragments. <i>Nucleic Acids Research</i> , 2008, 36, 2230-2239.	14.5	246
10	The genome of <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100 and its use for the reconstruction of metabolic pathways involved in xanthan biosynthesis. <i>Journal of Biotechnology</i> , 2008, 134, 33-45.	3.8	238
11	Complete genome of the mutualistic, N ₂ -fixing grass endophyte <i>Azoarcus</i> sp. strain BH72. <i>Nature Biotechnology</i> , 2006, 24, 1384-1390.	17.5	237
12	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. <i>Nature Communications</i> , 2014, 5, 5224.	12.8	236
13	Safety analysis of a Russian phage cocktail: From MetaGenomic analysis to oral application in healthy human subjects. <i>Virology</i> , 2013, 443, 187-196.	2.4	211
14	Comparative and Joint Analysis of Two Metagenomic Datasets from a Biogas Fermenter Obtained by 454-Pyrosequencing. <i>PLoS ONE</i> , 2011, 6, e14519.	2.5	208
15	Taxonomic composition and gene content of a methane-producing microbial community isolated from a biogas reactor. <i>Journal of Biotechnology</i> , 2008, 136, 91-101.	3.8	202
16	Oral T4-like phage cocktail application to healthy adult volunteers from Bangladesh. <i>Virology</i> , 2012, 434, 222-232.	2.4	201
17	TACO A – Taxonomic classification of environmental genomic fragments using a kernelized nearest neighbor approach. <i>BMC Bioinformatics</i> , 2009, 10, 56.	2.6	160
18	The Genome Sequence of the Tomato-Pathogenic Actinomycete <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> NCPPB382 Reveals a Large Island Involved in Pathogenicity. <i>Journal of Bacteriology</i> , 2008, 190, 2138-2149.	2.2	153

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19	Impact of Experimental Hookworm Infection on the Human Gut Microbiota. Journal of Infectious Diseases, 2014, 210, 1431-1434.	4.0	153
20	Vitamin D and the gut microbiome: a systematic review of in vivo studies. European Journal of Nutrition, 2019, 58, 2895-2910.	3.9	117
21	Infection with the carcinogenic liver fluke <i>Opisthorchis viverrini</i> modifies intestinal and biliary microbiome. FASEB Journal, 2013, 27, 4572-4584.	0.5	116
22	EMMA: a platform for consistent storage and efficient analysis of microarray data. Journal of Biotechnology, 2003, 106, 135-146.	3.8	100
23	Genome sequence of <i>Desulfobacterium autotrophicum</i> HRM2, a marine sulfate reducer oxidizing organic carbon completely to carbon dioxide. Environmental Microbiology, 2009, 11, 1038-1055.	3.8	100
24	Infections by human gastrointestinal helminths are associated with changes in faecal microbiota diversity and composition. PLoS ONE, 2017, 12, e0184719.	2.5	100
25	High fat diet drives obesity regardless the composition of gut microbiota in mice. Scientific Reports, 2016, 6, 32484.	3.3	97
26	Monozygotic twins affected with major depressive disorder have greater variance in methylation than their unaffected co-twin. Translational Psychiatry, 2013, 3, e269-e269.	4.8	89
27	Smchd1 regulates a subset of autosomal genes subject to monoallelic expression in addition to being critical for X inactivation. Epigenetics and Chromatin, 2013, 6, 19.	3.9	88
28	Genetic diversity and composition of a plasmid metagenome from a wastewater treatment plant. Journal of Biotechnology, 2008, 136, 65-76.	3.8	87
29	Hypermethylation in the ZBTB20 gene is associated with major depressive disorder. Genome Biology, 2014, 15, R56.	9.6	87
30	Experimental hookworm infection and escalating gluten challenges are associated with increased microbial richness in celiac subjects. Scientific Reports, 2015, 5, 13797.	3.3	86
31	Mapping the virome in wild-caught <i>Aedes aegypti</i> from Cairns and Bangkok. Scientific Reports, 2018, 8, 4690.	3.3	84
32	Suppression of inflammation by helminths: a role for the gut microbiota?. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140296.	4.0	78
33	Insight into the plasmid metagenome of wastewater treatment plant bacteria showing reduced susceptibility to antimicrobial drugs analysed by the 454-pyrosequencing technology. Journal of Biotechnology, 2008, 136, 54-64.	3.8	74
34	Genomic sequence of chorioallantois vaccinia virus Ankara, the ancestor of modified vaccinia virus Ankara. Journal of General Virology, 2007, 88, 3249-3259.	2.9	71
35	Pyrosequencing reveals transient cystic fibrosis lung microbiome changes with intravenous antibiotics. European Respiratory Journal, 2014, 44, 922-930.	6.7	71
36	Meta-analysis of the global gene expression profile of triple-negative breast cancer identifies genes for the prognostication and treatment of aggressive breast cancer. Oncogenesis, 2014, 3, e100-e100.	4.9	70

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37	Finding novel genes in bacterial communities isolated from the environment. <i>Bioinformatics</i> , 2006, 22, e281-e289.	4.1	68
38	Scabies Mites Alter the Skin Microbiome and Promote Growth of Opportunistic Pathogens in a Porcine Model. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2897.	3.0	67
39	BRAF mutation status is an independent prognostic factor for resected stage IIIB and IIIC melanoma: Implications for melanoma staging and adjuvant therapy. <i>European Journal of Cancer</i> , 2014, 50, 2668-2676.	2.8	67
40	Chromosome arm aneuploidies shape tumour evolution and drug response. <i>Nature Communications</i> , 2020, 11, 449.	12.8	65
41	Mothers Secretor Status Affects Development of Childrens Microbiota Composition and Function: A Pilot Study. <i>PLoS ONE</i> , 2016, 11, e0161211.	2.5	63
42	The Effects of Dietary Pattern during Intensified Training on Stool Microbiota of Elite Race Walkers. <i>Nutrients</i> , 2019, 11, 261.	4.1	62
43	Changes in duodenal tissue-associated microbiota following hookworm infection and consecutive gluten challenges in humans with coeliac disease. <i>Scientific Reports</i> , 2016, 6, 36797.	3.3	59
44	Analysis of the Effects of Dietary Pattern on the Oral Microbiome of Elite Endurance Athletes. <i>Nutrients</i> , 2019, 11, 614.	4.1	54
45	Identification of a Novel, EBV-Based Antibody Risk Stratification Signature for Early Detection of Nasopharyngeal Carcinoma in Taiwan. <i>Clinical Cancer Research</i> , 2018, 24, 1305-1314.	7.0	52
46	A comprehensive analysis of the faecal microbiome and metabolome of <i>Strongyloides stercoralis</i> infected volunteers from a non-endemic area. <i>Scientific Reports</i> , 2018, 8, 15651.	3.3	51
47	Whole-genome sequence of the bovine blood fluke <i>Schistosoma bovis</i> supports interspecific hybridization with <i>S. haematobium</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007513.	4.7	49
48	GISMO—gene identification using a support vector machine for ORF classification. <i>Nucleic Acids Research</i> , 2006, 35, 540-549.	14.5	47
49	Identification of the CIMP-like subtype and aberrant methylation of members of the chromosomal segregation and spindle assembly pathways in esophageal adenocarcinoma. <i>Carcinogenesis</i> , 2016, 37, 356-365.	2.8	46
50	Associations between micronutrient intakes and gut microbiota in a group of adults with cystic fibrosis. <i>Clinical Nutrition</i> , 2017, 36, 1097-1104.	5.0	46
51	REGANOR. <i>Applied Bioinformatics</i> , 2006, 5, 193-198.	1.6	44
52	Interspecific variations in the faecal microbiota of <i>Procellariiform</i> seabirds. <i>FEMS Microbiology Ecology</i> , 2014, 89, 47-55.	2.7	44
53	Neonatal environment exerts a sustained influence on the development of the intestinal microbiota and metabolic phenotype. <i>ISME Journal</i> , 2016, 10, 145-157.	9.8	44
54	Nutrigenomics: where are we with genetic and epigenetic markers for disposition and susceptibility?. <i>Nutrition Reviews</i> , 2010, 68, S38-S47.	5.8	42

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55	Influence of Fasting during Moulting on the Faecal Microbiota of Penguins. PLoS ONE, 2014, 9, e99996.	2.5	41
56	Infection with the sheep gastrointestinal nematode Teladorsagia circumcincta increases luminal pathobionts. Microbiome, 2020, 8, 60.	11.1	40
57	Genome-wide analysis of esophageal adenocarcinoma yields specific copy number aberrations that correlate with prognosis. Genes Chromosomes and Cancer, 2014, 53, 324-338.	2.8	38
58	Long-term Health-related Quality of Life Following Esophagectomy. Annals of Surgery, 2017, 265, 1158-1165.	4.2	38
59	Whole-genome sequence of the oriental lung fluke <i>Paragonimus westermani</i> . GigaScience, 2019, 8, .	6.4	29
60	Molecular investigation of bacterial communities on intravascular catheters: no longer just Staphylococcus. European Journal of Clinical Microbiology and Infectious Diseases, 2014, 33, 1189-1198.	2.9	26
61	Obesity-induced sperm DNA methylation changes at satellite repeats are reprogrammed in rat offspring. Asian Journal of Andrology, 2016, 18, 930.	1.6	26
62	Evaluation of the Microba Community Profiler for Taxonomic Profiling of Metagenomic Datasets From the Human Gut Microbiome. Frontiers in Microbiology, 2021, 12, 643682.	3.5	25
63	Whole-genome sequencing of human malignant mesothelioma tumours and cell lines. Carcinogenesis, 2019, 40, 724-734.	2.8	24
64	The Association between the Comprehensive Epstein-Barr Virus Serologic Profile and Endemic Burkitt Lymphoma. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 57-62.	2.5	23
65	Microbiota of little penguins and short-tailed shearwaters during development. PLoS ONE, 2017, 12, e0183117.	2.5	23
66	Building a BRIDGE for the integration of heterogeneous data from functional genomics into a platform for systems biology. Journal of Biotechnology, 2003, 106, 157-167.	3.8	22
67	Impact of Dietary Dairy Polar Lipids on Lipid Metabolism of Mice Fed a High-Fat Diet. Journal of Agricultural and Food Chemistry, 2013, 61, 2729-2738.	5.2	22
68	Mining, visualizing and comparing multidimensional biomolecular data using the Genomics Data Miner (GDMine) Web-Server. Scientific Reports, 2016, 6, 38178.	3.3	22
69	Increased susceptibility of airway epithelial cells from ataxia-telangiectasia to S. pneumoniae infection due to oxidative damage and impaired innate immunity. Scientific Reports, 2019, 9, 2627.	3.3	21
70	BRIGEP--the BRIDGE-based genome-transcriptome-proteome browser. Nucleic Acids Research, 2005, 33, W710-W716.	14.5	20
71	Helminths, polyparasitism, and the gut microbiome in the Philippines. International Journal for Parasitology, 2020, 50, 217-225.	3.1	20
72	Complex structural rearrangements are present in high-grade dysplastic Barrett's oesophagus samples. BMC Medical Genomics, 2019, 12, 31.	1.5	19

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73	Gastrointestinal Helminth Infection Improves Insulin Sensitivity, Decreases Systemic Inflammation, and Alters the Composition of Gut Microbiota in Distinct Mouse Models of Type 2 Diabetes. <i>Frontiers in Endocrinology</i> , 2020, 11, 606530.	3.5	17
74	Immune Signature Against <i>Plasmodium falciparum</i> Antigens Predicts Clinical Immunity in Distinct Malaria Endemic Communities. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 101-113.	3.8	16
75	Common variants in the CYP2C19 gene are associated with susceptibility to endometriosis. <i>Fertility and Sterility</i> , 2014, 102, 496-502.e5.	1.0	15
76	Patterns of Interindividual Variability in the Antibody Repertoire Targeting Proteins Across the Epstein-Barr Virus Proteome. <i>Journal of Infectious Diseases</i> , 2018, 217, 1923-1931.	4.0	13
77	Male-specific Association Between Fat-free Mass Index and Fecal Microbiota in 2- to 3-Year-Old Australian Children. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2018, 66, 147-151.	1.8	11
78	Chronic High-Fat Diet Induces Early Barrett's Esophagus in Mice through Lipidome Remodeling. <i>Biomolecules</i> , 2020, 10, 776.	4.0	10
79	Germline copy number variants are not associated with globally acquired copy number changes in familial breast tumours. <i>Breast Cancer Research and Treatment</i> , 2012, 134, 1005-1011.	2.5	7
80	Microbiota and Body Composition During the Period of Complementary Feeding. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2019, 69, 726-732.	1.8	6
81	Administration of Hookworm Excretory/Secretory Proteins Improves Glucose Tolerance in a Mouse Model of Type 2 Diabetes. <i>Biomolecules</i> , 2022, 12, 637.	4.0	6
82	Growth and protein-rich food intake in infancy is associated with fat-free mass index at 2-3 years of age. <i>Journal of Paediatrics and Child Health</i> , 2018, 54, 770-775.	0.8	4
83	Potential clinical utility of multiple target quantitative polymerase chain reaction (qPCR) array to detect microbial pathogens in patients with chronic obstructive pulmonary disease (COPD). <i>Journal of Thoracic Disease</i> , 2019, 11, S2254-S2265.	1.4	4
84	Practical Guide: Genomic Techniques and How to Apply Them to Marine Questions. , 2010, , 315-378.		0